

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana
Carroll, Joseph M.

<120> 23565, A NOVEL HUMAN ZINC
CARBOXYPEPTIDASE FAMILY MEMBER AND USES THEREOF

<130> 10448-142001

<150> 60/269,440

<151> 2001-02-16

<160> 6

<170> FastSEQ for Windows Version 4.0

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<211> 1687

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (160)...(1467)

<221> misc_feature

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cccaaggaaa gcccctgaag ctcaccagga ggaagaagc atg cag ggc act cct          174
                                   Met Gln Gly Thr Pro
                                   1              5

gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg acg ctc          222
Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg Thr Leu
                                   10              15              20

ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg aat ttc          270
Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met Asn Phe
                                   25              30              35

aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag cag ctt          318
Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys Gln Leu
                                   40              45              50

tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg gac ttc          366
Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val Asp Phe
                                   55              60              65

tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga gtt cct          414
Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg Val Pro

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2001-02-16

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				90									95					100	
gct	tac	agc	atc	atg	ata	aag	gac	atc	cag	gtg	ctg	ctg	gat	gag	gaa	510			
Ala	Tyr	Ser	Ile	Met	Ile	Lys	Asp	Ile	Gln	Val	Leu	Leu	Asp	Glu	Glu				
				105									110					115	
aga	cag	gcc	atg	gcg	aaa	tcc	cgc	cgg	ctg	gag	cgc	agc	acc	aac	agc	558			
Arg	Gln	Ala	Met	Ala	Lys	Ser	Arg	Arg	Leu	Glu	Arg	Ser	Thr	Asn	Ser				
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ttc	agt	tac	tca	tca	tac	cac	acc	ctg	gag	gag	ata	tat	agc	tgg	att	606			
Phe	Ser	Tyr	Ser	Ser	Tyr	His	Thr	Leu	Glu	Glu	Ile	Tyr	Ser	Trp	Ile				
				135													140	145	
gac	aac	ttt	gta	atg	gag	cat	tcc	gat	att	gtc	tca	aaa	att	cag	att	654			
Asp	Asn	Phe	Val	Met	Glu	His	Ser	Asp	Ile	Val	Ser	Lys	Ile	Gln	Ile				
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ggc	aac	agc	ttt	gaa	aac	cag	tcc	att	ctt	gtc	ctg	aag	ttc	agc	act	702			
Gly	Asn	Ser	Phe	Glu	Asn	Gln	Ser	Ile	Leu	Val	Leu	Lys	Phe	Ser	Thr				
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gga	ggt	tct	cgg	cac	cca	gcc	atc	tgg	atc	gac	act	gga	att	cac	tcc	750			
Gly	Gly	Ser	Arg	His	Pro	Ala	Ile	Trp	Ile	Asp	Thr	Gly	Ile	His	Ser				
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cgg	gag	tgg	atc	acc	cat	gcc	acc	ggc	atc	tgg	act	gcc	aat	aag	att	798			
Arg	Glu	Trp	Ile	Thr	His	Ala	Thr	Gly	Ile	Trp	Thr	Ala	Asn	Lys	Ile				
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gtc	agt	gat	tat	ggc	aaa	gac	cgt	gtc	ctg	aca	gac	ata	ctg	aat	gcc	846			
Val	Ser	Asp	Tyr	Gly	Lys	Asp	Arg	Val	Leu	Thr	Asp	Ile	Leu	Asn	Ala				
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atg	gac	atc	ttc	ata	gag	ctc	gtc	aca	aac	cct	gat	ggg	ttt	gct	ttt	894			
Met	Asp	Ile	Phe	Ile	Glu	Leu	Val	Thr	Asn	Pro	Asp	Gly	Phe	Ala	Phe				
				230													235	240	245
acc	cac	agc	atg	aac	cgc	tta	tgg	cgg	aag	aac	aag	tcc	atc	aga	cct	942			
Thr	His	Ser	Met	Asn	Arg	Leu	Trp	Arg	Lys	Asn	Lys	Ser	Ile	Arg	Pro				
				250													255	260	
gga	atc	ttc	tgc	atc	ggc	gtg	gat	ctc	aac	agg	aac	tgg	aag	tcg	ggt	990			
Gly	Ile	Phe	Cys	Ile	Gly	Val	Asp	Leu	Asn	Arg	Asn	Trp	Lys	Ser	Gly				
				265													270	275	
ttt	gga	gga	aat	ggt	tct	aac	agc	aac	ccc	tgc	tca	gaa	act	tat	cac	1038			
Phe	Gly	Gly	Asn	Gly	Ser	Asn	Ser	Asn	Pro	Cys	Ser	Glu	Thr	Tyr	His				
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ggg	ccc	tcc	cct	cag	tcg	gag	tcg	gag	gtg	gct	gcc	ata	gtg	aac	ttc	1086			
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Asp	Met	Arg	Val	Pro	Phe	Ser	Glu	Leu	Lys	Asp	Ile	Lys	Ala	Tyr	Leu
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Glu	Ser	His	Gly	Leu	Ala	Tyr	Ser	Ile	Met	Ile	Lys	Asp	Ile	Gln	Val

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 Leu Leu Asp Glu Glu Arg Gln Ala Met Ala Lys Ser Arg Arg Leu Glu
 115 120 125
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 130 135 140
 Ile Tyr Ser Trp Ile Asp Asn Phe Val Met Glu His Ser Asp Ile Val
 145 150 155 160
 Ser Lys Ile Gln Ile Gly Asn Ser Phe Glu Asn Gln Ser Ile Leu Val
 165 170 175
 Leu Lys Phe Ser Thr Gly Gly Ser Arg His Pro Ala Ile Trp Ile Asp
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 Thr Gly Ile His Ser Arg Glu Trp Ile Thr His Ala Thr Gly Ile Trp
 195 200 205
 Thr Ala Asn Lys Ile Val Ser Asp Tyr Gly Lys Asp Arg Val Leu Thr
 210 215 220
 Asp Ile Leu Asn Ala Met Asp Ile Phe Ile Glu Leu Val Thr Asn Pro
 225 230 235 240
 Asp Gly Phe Ala Phe Thr His Ser Met Asn Arg Leu Trp Arg Lys Asn
 245 250 255
 Lys Ser Ile Arg Pro Gly Ile Phe Cys Ile Gly Val Asp Leu Asn Arg
 260 265 270
 Asn Trp Lys Ser Gly Phe Gly Gly Asn Gly Ser Asn Ser Asn Pro Cys
 275 280 285
 Ser Glu Thr Tyr His Gly Pro Ser Pro Gln Ser Glu Ser Glu Val Ala
 290 295 300
 Ala Ile Val Asn Phe Ile Thr Ala His Gly Asn Phe Lys Ala Leu Ile
 305 310 315 320
 Ser Ile His Ser Tyr Ser Gln Met Leu Met Tyr Pro Tyr Gly Arg Leu
 325 330 335
 Leu Glu Pro Val Ser Asn Gln Arg Glu Leu Tyr Asp Leu Ala Lys Asp
 340 345 350
 Ala Val Glu Ala Leu Tyr Lys Val His Gly Ile Glu Tyr Ile Phe Gly
 355 360 365
 Ser Ile Ser Thr Thr Leu Tyr Val Ala Ser Gly Ile Thr Val Asp Trp
 370 375 380
 Ala Tyr Asp Ser Gly Ile Lys Tyr Ala Phe Ser Phe Glu Leu Arg Asp
 385 390 395 400
 Thr Gly Gln Tyr Gly Phe Leu Leu Pro Ala Thr Gln Ile Ile Pro Thr
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 Asn His Pro Tyr
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<211> 1311

<212> DNA

<213> Homo sapiens

<400> 3

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gatatgagag	ttcctttctc	cgaactgaaa	gacatcaaag	cttatctgga	gtctcatgga	300
cttgcttaca	gcatcatgat	aaaggacatc	caggtgctgc	tggaatgagga	aagacaggcc	360
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<212> PRT

<213> Artificial Sequence

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<223> Consensus sequence

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Gly Arg Asp Leu Lys Val Leu Lys Ile Ser Asp Asn Pro Ala Thr Gly
35     40     45
Glu Asn Glu Pro Glu Val Phe Ala Val Ala Gly Trp Ile His Ala Arg
50     55     60
Glu Trp Val Thr Ser Ala Thr Leu Leu Trp Leu Leu Lys Glu Leu Val
65     70     75     80
Ala Asn Tyr Gly Ser Asp Lys Thr Ile Thr Lys Leu Leu Asp Gly Leu
85     90     95
Asp Leu Phe Tyr Ile Leu Pro Val Phe Asn Pro Asp Gly Tyr Ala Tyr
100    105    110
Ser Ile Thr Thr Asp Ser Tyr Arg Met Trp Arg Lys Thr Arg Ser Pro
115    120    125
Asn Ala Gly Ser Phe Cys Val Gly Thr Asp Pro Asn Arg Asn Trp Tyr
130    135    140
Ala Gln Trp Gly Gly Met Gly Ala Ser Ser Tyr Ser Pro Cys Ser Glu
145    150    155    160
Thr Tyr Glu Gly Thr Ala Pro Phe Ser Glu Pro Glu Thr Lys Ala Val
165    170    175
Glu Asp Phe Ile Arg Ser Trp Leu Gly Gly Gly Lys Gln Asn Ile Lys
180    185    190
Ala Tyr Ile Thr Phe His Ser Tyr Ser Gln Leu Leu Leu Tyr Pro Tyr
195    200    205
Gly Tyr Asp Tyr Asn Leu Asn Pro Asp Ala Asn Asp Leu Asp Glu Leu
210    215    220
Ser Asp Leu Lys Ile Ala Ala Asp Ala Leu Ser Ala Arg His Gly Thr
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CCP-SE-001

[illegible]

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 35 40 45
 Pro Ala Glu Asp Ile Gln Ala Val Lys Ser Phe Leu Glu Gln Ser Gly
 50 55 60
 Ile His Tyr Glu Val Leu Ile Glu Asp Val Gln Glu Leu Leu Glu Glu
 65 70 75 80
 Gln Phe

203720-32592001